

GenCore version 5.1.6
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OM protein - protein search, using sw model

Run on: November 3, 2005, 08:43:50 ; Search time 168 Seconds
(Without alignments)
657,501 Million cell updates/sec

Title: US-10-813-549-1

Perfect score: 1380
Sequence: 1 MAISIKTPEDIEKRVAGRL.....CELLLRKDDTIPAIISHDE 264

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 1867879 seqs, 418409474 residues

Total number of hits satisfying chosen parameters: 1867879

Minimum DB seq length: 0
Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database :

- Published Applications AA:*
- 1: /cgn2_6/ptodata/1/pubppaa/US07_PUBCOMB.pep.*
 - 2: /cgn2_6/ptodata/1/pubppaa/PCT_NEW_PUB.pep.*
 - 3: /cgn2_6/ptodata/1/pubppaa/US06_NEW_PUB.pep.*
 - 4: /cgn2_6/ptodata/1/pubppaa/US06_PUBCOMB.pep.*
 - 5: /cgn2_6/ptodata/1/pubppaa/US07_NEW_PUB.pep.*
 - 6: /cgn2_6/ptodata/1/pubppaa/PCTUS_PUBCOMB.pep.*
 - 7: /cgn2_6/ptodata/1/pubppaa/US08_NEW_PUB.pep.*
 - 8: /cgn2_6/ptodata/1/pubppaa/US08_PUBCOMB.pep.*
 - 9: /cgn2_6/ptodata/1/pubppaa/US09_PUBCOMB.pep.*
 - 10: /cgn2_6/ptodata/1/pubppaa/US09_PUBCOMB.pep.*
 - 11: /cgn2_6/ptodata/1/pubppaa/US09_PUBCOMB.pep.*
 - 12: /cgn2_6/ptodata/1/pubppaa/US09_NEW_PUB.pep.*
 - 13: /cgn2_6/ptodata/1/pubppaa/US10_PUBCOMB.pep.*
 - 14: /cgn2_6/ptodata/1/pubppaa/US10_PUBCOMB.pep.*
 - 15: /cgn2_6/ptodata/1/pubppaa/US10_PUBCOMB.pep.*
 - 16: /cgn2_6/ptodata/1/pubppaa/US10_PUBCOMB.pep.*
 - 17: /cgn2_6/ptodata/1/pubppaa/US10_PUBCOMB.pep.*
 - 18: /cgn2_6/ptodata/1/pubppaa/US10_PUBCOMB.pep.*
 - 19: /cgn2_6/ptodata/1/pubppaa/US11_PUBCOMB.pep.*
 - 20: /cgn2_6/ptodata/1/pubppaa/US11_NEW_PUB.pep.*
 - 21: /cgn2_6/ptodata/1/pubppaa/US60_NEW_PUB.pep.*
 - 22: /cgn2_6/ptodata/1/pubppaa/US60_PUBCOMB.pep.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	1380	100.0	264	15	US-10-299-867-12
2	1380	100.0	264	17	US-10-350-516-8
3	1380	100.0	264	17	US-10-893-671-31
4	1380	100.0	264	18	US-10-813-549-1
5	1371	99.3	263	15	US-10-350-516-9
6	910.5	66.0	268	15	US-10-299-867-13
7	910.5	66.0	268	18	US-10-958-216-121
8	909.5	65.9	261	18	US-10-958-216-59
9	909.5	65.9	261	18	US-10-958-216-61
10	904.5	65.5	268	18	US-10-958-216-123
11	669.5	48.5	253	15	US-10-299-867-10

12	669.5	48.5	253	15	US-10-350-516-4	Sequence 4, Appl1
13	646	46.8	274	15	US-10-299-867-11	Sequence 11, Appl1
14	619	44.9	285	14	US-10-156-761-13458	Sequence 13458, A
15	617.5	44.7	391	16	US-10-425-115-299292	Sequence 299292, A
16	614	44.5	394	15	US-10-299-867-2	Sequence 2, Appl1
17	614	44.5	394	15	US-10-350-516-3	Sequence 3, Appl1
18	614	44.5	394	16	US-10-723-860-1103	Sequence 1103, Ap
19	614	44.5	494	15	US-10-399-645-13	Sequence 13, Appl1
20	595.5	43.2	263	9	US-09-738-626-5698	Sequence 5698, Ap
21	595	43.1	374	20	US-11-097-143-31929	Sequence 31929, A
22	590	42.8	248	18	US-10-510-812-34	Sequence 34, Appl1
23	587	42.5	397	15	US-10-424-599-247413	Sequence 247413, A
24	583	42.2	248	15	US-10-299-867-15	Sequence 15, Appl1
25	574.5	41.6	371	14	US-10-032-585-7897	Sequence 7897, Ap
26	565.5	41.0	348	16	US-10-425-115-185115	Sequence 185115, A
27	565	40.9	305	15	US-10-299-867-17	Sequence 17, Appl1
28	565	40.9	305	15	US-10-350-516-7	Sequence 7, Appl1
29	562.5	40.8	364	15	US-10-425-114-64761	Sequence 64761, A
30	559.5	40.5	367	15	US-10-299-867-9	Sequence 9, Appl1
31	557.5	40.4	346	16	US-10-437-963-150622	Sequence 150622, A
32	556.5	40.3	369	15	US-10-042-865-187	Sequence 187, App
33	552.5	40.0	369	15	US-10-042-865-187	Sequence 187, App
34	550.5	39.9	365	15	US-10-424-599-173546	Sequence 173546, A
35	547.5	39.7	341	16	US-10-425-115-353435	Sequence 353435, A
36	543.5	39.4	373	16	US-10-437-963-170579	Sequence 170579, A
37	539	39.1	294	15	US-10-289-762-1081	Sequence 1081, Ap
38	531.5	38.5	382	15	US-10-424-599-244001	Sequence 244001, A
39	519	37.6	254	18	US-10-958-216-103	Sequence 103, App
40	518.5	37.6	307	15	US-10-042-865-188	Sequence 188, App
41	518.5	37.6	307	20	US-11-097-143-10797	Sequence 10797, A
42	518.5	37.6	350	16	US-10-425-115-299386	Sequence 299386, A
43	516	37.4	262	18	US-10-501-282-3480	Sequence 3480, Ap
44	515	37.3	254	18	US-10-958-216-105	Sequence 105, Appl
45	501	36.3	306	15	US-10-425-114-58168	Sequence 58168, A

ALIGNMENTS

RESULT 1
US-10-299-867-12
; Sequence 12, Application US/10299867
; General Information:
; Application No. US20030203406A1
; APPLICANT: Symson, Carolyn J.
; APPLICANT: Dotsen, Stancov B.
; APPLICANT: Frazier, Ronald B.
; APPLICANT: Woods, Cynthia L.
; APPLICANT: Zakeri, Hamideh
; APPLICANT: Zhou, Xianzhi
; TITLE OF INVENTION: Human methionine aminopeptidase type 3
; FILE REFERENCE: S03181-01-US
; CURRENT APPLICATION NUMBER: US/10/299,867
; PRIOR FILING DATE: 2002-11-19
; PRIOR APPLICATION NUMBER: US 60/125,139
; PRIOR FILING DATE: 1999-03-11
; PRIOR APPLICATION NUMBER: US 09/523,263
; NUMBER OF SEQ ID NOS: 69
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 12
; LENGTH: 264
; TYPE: PRT
; ORGANISM: E. coli Metap

Query Match 100.0% ; Score 1380; DB 15; Length 264;
Best Local Similarity 100.0% ; Pred. No. 2,2e+13;
Matches 264; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MAISIKTPEDIEKRVAGRLAEVLEMIPEYKPGVSTGELDRICNDYIVNEQHAVSACL 60

OM protein - protein search, using sw model

Run on: November 3, 2005, 08:31:04 ; Search time 175 Seconds
(without alignments)
772.508 Million cell updates/sec

Title: US-10-813-549-1

Perfect score: 1380
Sequence: 1 MAISIKTPEDIEKRVAGRL.....CELLTKRDKPTPAISHDE 264

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 1612378 segs, 512079187 residues

Total number of hits satisfying chosen parameters: 1612378

Minimum DB seq length: 0
Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : UniProt_03:*
1: uniprot_sprot:*
2: uniprot_crembl:*

Prod. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	1380	100.0	264	1 AMPM_ECOLI	P07906 escherichia
2	1253	90.8	263	1 AMPM_SALTY	P10882 salmonella
3	1198	86.8	263	2 O66718	O66718 yersinia pe
4	1195	86.6	263	2 O82H67	O82H67 yersinia pe
5	1158	83.9	264	2 O6DBE4	O6DBE4 erwinia car
6	1137.5	82.4	265	2 O7N8P8	O7N8P8 photorhabdu
7	946	68.6	267	2 O9CNH2	O9CNH2 pasteurilla
8	937	67.9	264	1 AMPM_BUCAI	P57324 buchera ap
9	934	67.7	268	2 O7VP53	O7VP53 haemophilus
10	919.5	66.6	260	2 O886P4	O886P4 pseudomonas
11	915	66.3	264	2 O7VR87	O7VR87 pseudomonas
12	910.5	66.0	268	1 AMPM_HARIN	O88MI1 pseudomonas
13	909.5	65.9	261	2 O9HXT1	P44421 haemophilus
14	902	65.4	261	1 AMPM_BUCAP	O9HXY1 pseudomonas
15	886.5	64.2	270	2 O65S27	O8K9C1 buchera ap
16	881	63.8	258	2 O83BV1	O65S27 manheimia
17	880.5	63.6	275	2 O6LN23	O83BV1 coxiella bu
18	878	63.3	258	2 O8PMW9	O6LN23 photobacter
19	874	63.3	258	2 O8PAU5	O8PMW9 xanthomonas
20	853	61.8	259	2 O7QMK0	O8PAU5 xanthomonas
21	853	61.8	259	2 O87F52	O7QMK0 anopheles g
22	852	61.7	259	2 O9PH35	O87F52 xylella fas
23	849.5	61.6	266	1 AMPM_BUCBP	O9PH35 xylella fas
24	849.5	61.6	266	1 O8EGH7	O8EGH7 wiggleswort
25	843.5	59.7	260	2 O9KPEV1	O89AP3 buchera ap
26	834	58.3	272	2 O82XJ5	O89AP3 shewanella
27	804	57.8	271	2 O62JC3	O9KPEV1 vibrio chol
28	798	57.8	271	2 O63T11	O82XJ5 nitrosomonas
29	796.5	57.7	261	2 O66E99	O63T11 burkholderi
30					O66E99 yersinia ps

ALIGNMENTS

RESULT 1									
ID	AMPM_ECOLI	STANDARD	PRT	264 AA.					
AC	P07906								
DT	01-AUG-1988 (Rel. 08, Created)								
DT	01-AUG-1988 (Rel. 08, Last sequence update)								
DT	25-JAN-2005 (Rel. 46, Last annotation update)								
DE	Methionine aminopeptidase (EC 3.4.11.18) (MAP) (Peptidase M).								
GN	Name=map								
GN	OrderedLocustNames=b0168, c0203, z0178, EC60170, SF0158, S0161.								
OS	Escherichia coli								
OS	Escherichia coli O6,								
OS	Escherichia coli O157:H7, and								
OS	Shigella flexneri.								
OC	Bacteria; Proteobacteria; Gammaproteobacteria; Enterobacteriales;								
OC	Enterobacteriaceae; Escherichia.								
OX	NCBI_TaxID=562, 217992, 83334, 623;								
RP	[1]								
RP	SEQUENCE FROM N.A.								
RC	SPECIES=E.coli;								
RX	MEDLINE=87109068; PubMed=3027045;								
RA	Ben-Bassat A., Bauer K., Chang S.-Y., Myambo K., Boosman A., Chang S.,								
RT	"Processing of the initiation methionine from proteins: properties of								
RT	the Escherichia coli methionine aminopeptidase and its gene								
RL	structure.";								
RL	J. Bacteriol. 169:751-757(1987).								
RN	[2]								
RP	SEQUENCE FROM N.A.								
RC	SPECIES=E.coli; STRAIN=KL2 / W3110;								
RX	MEDLINE=97426617; PubMed=9278503; DOI=10.1126/science.277.5331.1453;								
RA	Baltner F.R., Plunkett G. III, Bloch C.A., Perna N.T., Burland V.,								
RT	Riley M., Collado-Vides J., Glasner J.D., Rode C.K., Mayhew G.F.,								
RT	Gregor J., Davis N.W., Kirkpatrick H.A., Goeden M.A., Rose D.J.,								
RT	Mau B., Shao Y.;								
RL	"The complete genome sequence of Escherichia coli K-12.";								
RL	Science 277:1453-1474(1997).								
RN	[4]								
RP	SEQUENCE FROM N.A.								
RC	SPECIES=E.coli;								
RX	Schramm S., Duncan M., Allen E., Araujo R., Aparicio A., Chung E.,								
RA	Davis K., Federspiel N., Hyman R., Kalman S., Komp C., Kurdi O.,								
RT	Lashari D., Lew H., Lin D., Namath A., Oefner P., Roberts D.,								
RT	Davis R.W.;								
RL	Submitted (SEP-1996) to the EMBL/GenBank/DBJ databases.								
RP	[5]								
RP	SEQUENCE FROM N.A.								

32	796.5	57.7	261	2	O8ZBR7	O8ZBR7 yersinia pe
33	795	57.6	265	2	O7NVE6	O7NVE6 chromobacte
34	791	57.3	275	2	O8XZJ2	O8XZJ2 ralsstona s
35	779.5	56.5	254	2	O6FA52	O6FA52 acinetobact
36	775.5	56.2	292	2	O87MD7	O87MD7 vibrio para
37	775	56.2	263	2	O883J5	O883J5 pseudomonas
38	765.5	55.5	292	2	O8DBG2	O8DBG2 vibrio vuln
39	763.5	55.3	292	2	O7MTF9	O7MTF9 acinetobact
40	761	55.1	265	2	O6FAN1	O6FAN1 neisseria m
41	758.5	55.0	259	2	O9JXD9	O9JXD9 neisseria m
42	758.5	55.0	263	2	O7NWX8	O7NWX8 chromobacte
43	746	54.1	260	2	O73J14	O73J14 wolbachia p
44	745.5	54.0	260	2	O7VYD1	O7VYD1 bordetella
45	743	53.8	273	2		

OM protein - protein search, using sw model

Run on: November 3, 2005, 08:34:05 ; Search time 40 Seconds
(without alignments)
635,031 Million cell updates/sec

Title: US-10-813-549-1

Sequence: 1 MAISTKPEDIEKRRVAGRL.....CEILTKRKDPTIPAIISHDE 264

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 283416 seqs, 96216763 residues

Total number of hits satisfying chosen parameters: 283416

Minimum DB seq length: 0
Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : PIR 79:*

1: p1r1:*

2: p1r2:*

3: p1r3:*

4: p1r4:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	1380	100.0	264	1 DPECM	methionyl aminopep
2	1380	100.0	264	2 B85501	methionine aminope
3	1380	100.0	264	2 B90650	methionine aminope
4	1258	91.2	264	2 A10528	methionine aminope
5	1258	91.2	264	2 S12027	methionyl aminope
6	1195	86.6	263	2 AB0128	methionyl aminope
7	937	67.9	264	2 A64957	methionyl aminope
8	910.5	66.0	268	2 C64138	methionyl aminope
9	909.5	65.9	261	2 D83189	methionine aminope
10	852	61.7	259	2 B82845	methionine aminope
11	823.5	59.7	280	2 D82097	methionine aminope
12	796.5	57.7	261	2 AB0405	methionyl aminope
13	758.5	55.0	259	2 B82029	methionyl aminope
14	758.5	55.0	259	2 C81008	methionine aminope
15	739	53.6	260	2 C83301	probable methionin
16	723.5	52.4	256	2 AG2334	methionine aminope
17	687	50.5	276	2 H87380	methionine aminope
18	685.5	49.7	259	2 A71644	methionine aminope
19	684.5	49.6	259	2 D97858	methionyl aminope
20	669.5	48.5	253	2 S75731	methionyl aminope
21	660	47.8	278	2 AB2774	methionyl aminope
22	660	47.8	278	2 H97553	methionine aminope
23	659	47.8	276	2 A13341	methionyl aminope
24	646	46.8	274	2 S76999	methionyl aminope
25	634	45.9	285	2 B87106	methionine aminope
26	630	45.7	285	2 T50575	methionyl aminope
27	617	44.7	285	2 G70885	probable map prote
28	584	43.0	398	2 B84888	probable methionin
29	592	42.9	259	2 C75410	methionine aminope

30	583	42.2	248	2 JS0493	methionyl aminope
31	568	41.2	275	2 AH1933	methionine aminope
32	565	40.9	305	2 S75743	methionyl aminope
33	559.5	40.5	387	2 S59390	methionyl aminope
34	557.5	40.4	250	2 F72247	methionine aminope
35	556.5	40.3	369	2 C86267	probable methionin
36	553.5	40.1	305	2 E85437	methionyl aminope
37	549	39.8	295	2 G81724	methionine aminope
38	543	39.3	291	2 D71462	probable methionin
39	540	39.1	248	2 T44405	methionyl aminope
40	539	39.1	266	2 A81531	methionine aminope
41	539	39.1	291	2 F86616	methionine aminope
42	539	39.1	291	2 E72008	methionine aminope
43	532	38.6	279	2 T40384	probable methionin
44	488.5	35.4	358	2 F70307	methionyl aminope
45	482	34.9	252	2 AD1660	methionine aminope

ALIGNMENTS

RESULT 1
DPECM
methionyl aminopeptidase (EC 3.4.11.18) [validated] - Escherichia coli (strain K-12)
N/Alternate names: metallooligopeptidase; methionine aminopeptidase; peptidase M
C/Species: Escherichia coli
C/Date: 30-Sep-1988 #sequence revision 30-Sep-1988 #text_change 09-Jul-2004
C/Accession: A27761; S45233; H64740
R/Ben-Bassat, A.; Bauer, K.; Chang, S.Y.; Myambo, K.; Boosmaier, A.; Chang, S.
J. Bacteriol. 169, 751-757, 1987
A/Title: Processing of the initiation methionine from proteins: properties of the Esche
A/Reference number: A27761; MUID:87109068; PMID:3027045
A/Molecule type: DNA
A/Residues: 1-264 <BEN>
A/Cross-references: UNIPROT:P07906; GB:M15106; NID:9146726; PIDN:AAA24112.1; PID:914672
A/Note: Comparative analyses indicate that residues adjacent to initial methionines of
R.Fujita, N.
submitted to the EMBL Data Library, January 1994
A/Reference number: S45181
A/Accession: S45233
A/Molecule type: DNA
A/Residues: 1-264 <FUJ>
A/Cross-references: EMBL:D26562; NID:9473770; PIDN:BA05612.1; PID:9473823
A/Experimental source: strain K-12, substrain W3110
R/Blahtner, F.R.; Plunkett III, G.; Bloch, C.A.; Perna, N.T.; Burland, V.; Riley, M.; C
.A.; Rose, D.J.; Mau, B.; Shao, Y.
Science 277, 1453-1462, 1997
A/Title: The complete genome sequence of Escherichia coli K-12.
A/Reference number: A64720; MUID:97426617; PMID:9278503
A/Accession: H64740
A/Status: nucleic acid sequence not shown; translation not shown
A/Molecule type: DNA
A/Residues: 1-264 <BLAT>
A/Cross-references: GB:AE000126; GB:U00096; NID:91786358; PIDN:AACT3279.1; PID:91786364;
A/Experimental source: strain K-12, substrain MG1655
R/Roderick, S.L.; Matthews, B.W.
submitted to the Brookhaven Protein Data Bank, December 1992
A/Reference number: A51847; PDB:1WAT
A/Contents: annotation; X-ray crystallography, 2.4 angstroms, residues 2-264
R/Roderick, S.L.; Matthews, B.W.
Biochemistry 32, 3907-3912, 1993
A/Title: Structure of the cobalt-dependent methionine aminopeptidase from Escherichia co
A/Reference number: A49470; MUID:93229467; PMID:8471602
A/Contents: annotation; X-ray crystallography, 2.4 angstroms
C/Genetics:
A/Map position: 4 min
C/Complex: monomer
C/Function:
A/Description: catalyzes hydrolysis of amino-terminal methionine from proteins
C/Superfamily: Escherichia coli methionyl aminopeptidase
C/Keywords: aminopeptidase; cobalt; metalloprotein; monomer; protein biosynthesis

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OM protein - nucleic search, using frame_plus.p2n model

Run on: November 11, 2005, 18:02:50 ; Search time 2355 Seconds
(without alignments)
4267.077 Million cell updates/sec

Title: US-10-813-549-1

Perfect score: 1380
Sequence: 1 MAISIKTPEIDIEKMKVAGRL.....CEILTLRKDDITPATISDE 264

Scoring table: BLOSUM62
Xgapop 10.0 , Xgapext 0.5
Ygapop 10.0 , Ygapext 0.5
Fgapop 6.0 , Fgapext 7.0
Delop 6.0 , Delext 7.0

Searched: 34339544 seqs, 19032134700 residues

Total number of hits satisfying chosen parameters: 68479088

Minimum DB seq length: 0
Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Command line parameters:
-MODEL=frame+ p2n.model -DEV=xlh
-Q=cgnt_1/USPTO.spool/US10813549/runat_03112005_075935_13175/app_query.fasta_1.455
-DB=EST -QMT=fastlap -SUFF1=1 -END=1 -MATRIX=biosum62 -TRANS=human40.cdi -LIST=45
-UNITS-bits -START=1 -BND=1 -THR MAX=100 -THR MIN=0 -ALIGN=20 -MODE=LOCAL
-DOCALLIGN=200 -THR SCORE=pct -THR MAX=100 -THR MIN=0 -ALIGN=20 -MODE=LOCAL
-OUTFMT=pico -NORM=ext -HEAPSIZE=500 -MINLEN=0 -MAXLEN=200000000
-USRR=US10813549 @CGN 1 1 3437 @runat_03112005_075935_13175 -NCPU=6 -ICPU=3
-NO_MMAP -LARGEOUTRY -NEG_SCORES=0 -WAIT -DSPBLCK=100 -LONGLOG
-DEV_TIMEOUT=120 -WARN_TIMEOUT=30 -THREADS=1 -XGAPOP=10 -XGAPEXT=0.5 -Fgapop=6
-FGAPEXT=7 -YGAPOP=10 -YGAPEXT=0.5 -DELOP=6 -DELEX=7

Database : EST:
1: gb_est1.*
2: gb_est2.*
3: gb_hlc.*
4: gb_est3.*
5: gb_est4.*
6: gb_est5.*
7: gb_est6.*
8: gb_gss1.*
9: gb_gss2.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	1351	97.9	812	9	CL661282 PRI0139b
2	1327	96.2	844	9	CL668009 PRI0148b
3	1236	89.6	716	9	CL663485 PRI0144b
4	793.5	57.5	830	1	AL669413 AL669413
5	786	57.0	706	8	AQ989727 RfC00360
6	756	54.8	839	9	CL666394 PRI0152b
7	614	44.5	1047	9	AY420765 Homo sapi
8	607	44.0	1335	9	CR696222 Tetradon
9	605	43.8	1047	9	AY420767 Mus muscu

10	605	43.8	2550	3	AK077694
11	604	43.7	1864	3	CR694735
12	603	43.7	870	7	CO163928 FLD1_44_E
13	601	43.6	739	9	CL685899 PRI0142b
14	599	43.4	631	8	BH762604 BMBAC330A
15	599	43.4	995	9	AY420766 Rn trogl
16	594	43.0	1308	3	CR688406
17	585	42.4	926	5	BQ706230
18	578	41.9	890	7	CK458575
19	573	41.5	859	5	BQ232415
20	569.5	41.3	967	3	AK006484
21	568	41.2	940	5	BQ937757
22	561.5	40.7	997	7	CR264740
23	560.5	40.6	780	8	BZ573414
24	558.5	40.5	867	7	CF205959
25	558.5	40.5	885	7	CF514702
26	556.5	40.3	1235	3	CNS04BLO
27	549.5	39.8	876	5	BUI36049
28	548.5	39.7	1278	3	CNS0A285
29	547	39.6	742	4	BQ434305
30	547	39.6	760	4	BQ432312
31	545	39.5	888	7	CN159313
32	542.5	39.3	637	1	AJ722958
33	542.5	39.3	818	7	CO978868
34	541	39.2	682	6	CD717720
35	541	39.2	761	4	BQ434187
36	540.5	39.2	1347	8	BZ54793
37	537.5	38.9	915	7	CK269489
38	533	38.6	778	7	CN359624
39	532.5	38.6	898	7	CY243178
40	530.5	38.4	989	7	CO025828
41	528	38.3	715	4	BQ435572
42	527.5	38.2	684	2	BB468358
43	527.5	38.2	797	2	BB902721
44	526	38.1	722	6	CA239368
45	526	38.1	731	1	AV881422

ALIGNMENTS

RESULT 1
LOCUS CL661282 812 bp DNA linear GSS 09-JUN-2004
DEFINITION PRI0139b.G03 - PRI0139b.B21 (812) Mixed stage fosmid library of P. pacificus var. California Pristionchus pacificus genomic, genomic survey sequence.

ACCESSION CL661282.1 GI:50147601
VERSION
KEYWORDS
SOURCE
ORGANISM

REFERENCE
AUTHORS
TITLE
JOURNAL
COMMENT

1 (bases 1 to 812)
Strinivasan, J., Otto, G.W., Kahlow, U., Geisler, R. and Sommer, R.J.
Appabi: an Acedb database for the nematode satellite organism
Pristionchus pacificus
Nucleic Acids Res. 32 (1), D421-D422 (2004)
Contact: Sommer, R.J.
Evolutionary Biology
Max-Planck-Institute for Developmental Biology
Spemannstr. 37-39, Tuebingen D-72076, Germany
Tel: 00497071601371
Fax: 00497071601498
Email: ralf.sommer@tuebingen.mpg.de
This library was generated at Caltech, Pasadena, USA and end
sequenced at Vancouver, Canada.
Seq primer: T7
Class: fosmid ends.

FEATURES
source
1..812
/organism="Pristionchus pacificus"
/mol_type="genomic DNA"

OM protein - nucleic search, using frame_plus_g2n model

Run on: November 11, 2005, 16:26:32 ; Search time 3123 Seconds

(Without alignments)
4096.118 Million cell updates/sec

Title: US-10-813-549-1
Perfect score: 1380
Sequence: 1 MAISIKTPEDIEKREAVAGRL.....CELTURKDDTTPAISHDE 264

Scoring table:

BLOSUM62
Xgapop 10.0 , Xgapext 0.5
Ygapop 10.0 , Ygapext 0.5
Fgapop 6.0 , Fgapext 7.0
Delop 6.0 , Delext 7.0

Searched: 4708233 seqs, 24227607955 residues

Total number of hits satisfying chosen parameters: 9416466

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Command line parameters:
-MODEL=frame+g2n.model -DEV=x1h
-Q=/cgm2_1/USPTO.spool/US10813549/runat.03112005.075935.13164/app.query.fasta.1.455
-DB=genemb1 -QMT=fastap -SUFFIX=rge -MINMATCH=0.1 -LOOFC=0 -LOOEXT=0
-UNITS=bits -START=1 -END=1 -MATRIX=biosum62 -TRANS=human40.cdi -LIST=45
-DOCALLIGN=200 -THR_SCORE=pct -THR_MAX=100 -THR_MIN=0 -ALIGN=20 -MODE=LOCAL
-OUTMT=ptc -NORM=ext -HEAPSIZ=500 -MINLEN=0 -MAXLEN=2000000000
-USER=US10813549 @CGN 1 1 3731 @runat.03112005.075935.13164 -NCPU=6 -ICPU=3
-NO MMAP -LARGEQUERY -NEG_SCORES=0 -WRT -DSPLOCK=100 -LONGLOG
-DEV TIMEOUT=120 -WARN TIMEOUT=30 -THREADS=1 -XGAPOP=10 -XGAPEXT=0.5 -Fgapop=6
-Fgapext=7 -YGAPOP=10 -YGAPEXT=0.5 -DELop=6 -DELEXT=7

Database :

Genemb1:*
1: gb_ba:*
2: gb_hcg:*
3: gb_in:*
4: gb_on:*
5: gb_ov:*
6: gb_pat:*
7: gb_ph:*
8: gb_pl:*
9: gb_pr:*
10: gb_ro:*
11: gb_sts:*
12: gb_sy:*
13: gb_un:*
14: gb_vi:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	1380	100.0	1197	1	ECOMAP
2	1380	100.0	1197	6	E01194
3	1380	100.0	1197	6	E01194
4	1380	100.0	1197	6	E01194

C 5	1380	100.0	11204	6	AX370213	AX370213 Sequence
C 6	1380	100.0	13945	1	AE015052	AE015052 Shigella
C 7	1380	100.0	14042	1	AE005192	AE005192 Escherich
C 8	1380	100.0	82727	1	EC082K	D26562 Escherich
C 9	1380	100.0	110000	1	U00096_01	Continuation (2 of
C 10	1380	100.0	123171	1	EC070214	U70214 Escherichia
C 11	1380	100.0	281530	1	AP002550	AP002550 Escherich
C 12	1380	100.0	290029	1	AE016978	AE016978 Shigella
C 13	1380	100.0	300409	1	AE016755	AE016755 Escherich
C 14	1380	100.0	303656	2	AC025528	AC025528 Mus muscu
C 15	1330	96.4	846	6	AR388489	AR388489 Sequence
C 16	1325	96.0	3779	1	EC06LNA	X55778 S. typhimur
C 17	1258	91.2	1811	1	STREPMM	K96431 Escherichia
C 18	1258	91.2	19971	1	AE008704	AE008704 Salmonell
C 19	1258	91.2	251050	1	AL627265	AL627265 Salmonell
C 20	1258	91.2	300169	1	AE016834	AE016834 Salmonell
C 21	1198	86.8	110000	1	BX36398_35	Continuation (36 o
C 22	1195	86.6	10443	1	AE013914	AE013914 Yersinia
C 23	1195	86.6	210050	1	AE014146	AE014146 Yersinia
C 24	1195	86.6	291817	1	AE017137	AE017137 Yersinia
C 25	1158	83.9	110000	1	BX950851_11	Continuation (12 o
C 26	1137.5	82.4	342905	1	BX571861	BX571861 Phototrab
C 27	1137.5	82.4	349980	6	AX770908	AX770908 Sequence
C 28	1086	78.7	807	6	AR377418	AR377418 Sequence
C 29	946	68.6	11341	1	AE006081	AE006081 Pasteurel
C 30	937	67.9	110000	6	AR409405_2	Continuation (3 of
C 31	937	67.9	110000	6	BD061520_2	Continuation (3 of
C 32	937	67.9	347550	1	AE001118	AE001118 Buchnera
C 33	934	67.7	304558	1	AE017151	AE017151 Haemophil
C 34	919.5	66.6	310029	1	AE016861	AE016861 Pseudomon
C 35	915	66.3	267050	1	BX248585	BX248585 Blochmann
C 36	914.5	66.3	301995	1	AE016779	AE016779 Pseudomon
C 37	911.5	66.1	308766	6	CO873161	CO873161 Sequence
C 38	910.5	66.0	807	6	AX928193	Continuation (18 o
C 39	910.5	66.0	11782	1	U32845	Continuation (18 o
C 40	910.5	66.0	110000	6	BD426631_17	Continuation (18 o
C 41	910.5	66.0	110000	6	AR274513_17	Continuation (18 o
C 42	910.5	66.0	110000	6	AR541453_17	Continuation (18 o
C 43	909.5	65.9	786	6	AX928131	AX928131 Sequence
C 44	909.5	65.9	786	6	AX928133	AX928133 Sequence
C 45	909.5	65.9	14537	1	AE004785	AE004785 Pseudomon

ALIGNMENTS

RESULT 1	ECOMAP	1197 bp	DNA	linear	BCI 26-APR-1993
LOCUS	E.coli map gene, encoding methionine amino peptidase, complete cds.				
DEFINITION	ACCESSION	VERSION	KEYWORDS	SOURCE	ORGANISM
M5106	M5106.1	GI:146726	map gene; metallo-oligopeptidase; methionine aminopeptidase.	Escherichia coli	Escherichia coli
REFERENCE	AUTHORS	TITLE	JOURNAL	MEDLINE	PUBMED
1 (bases 1 to 1197)	Ben-Bassat,A., Bauer,K., Chang,S.Y., Myambo,K., Boosman,A. and Chang,S.	Processing of the initiation methionine from proteins: properties of the Escherichia coli methionine aminopeptidase and its gene structure	J. Bacteriol.	169 (2), 751-757 (1987)	3027045
Original source text: E.coli (strain CW89) DNA, clone pSYC1174. Draft entry and computer-readable sequence for [1] kindly provided by S.Chang, 01-JUN-1987.		There are at least two tandem 'map' gene promoters separated by the SnaI site at positions 150. Two regions of dyad symmetry are located at positions 187-201 and 1018-1037.			
Location/Qualifiers					
1.	1197				

OM protein - nucleic search, using frame_plus_p2n model

Run on: November 11, 2005, 18:29:14 ; Search time 621 Seconds

(without alignments)
3515,672 Million cell updates/sec

Title: US-10-813-549-1
Perfect score: 1380
Sequence: 1 MA5IKTPEIDKRVAVGRL.....CEITLRKDTTIPAIISHDE 264

Scoring table:
BLOSUM62
Xgapop 10.0, Xgapext 0.5
Ygapop 10.0, Ygapext 0.5
Fgapop 6.0, Fgapext 7.0
Delop 6.0, Delext 7.0

Searched: 9794790 seqs, 413490567 residues

Total number of hits satisfying chosen parameters: 19589580

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Command line parameters:
-MODE=frame+ p2n.model -DEV=x1h
-Q=/cgn2_1/USPTO.spool/US10813549/runat_03112005_075936_13214/app_query.fasta_1.455
-DB=Published Applications NA -OFMT=fastap -SUFFIX=rpdb -MINMATCH=0.1
-LOOPEXT=0 -UNITS=bits -START=1 -END=1 -MATRIX=blowsum62
-TRANS=human40.csi -LIST=45 -DOCALL=200 -THR_SCORE=pct -THR_MAX=100
-THR_MIN=0 -ALIGN=20 -MODS=JOCAL -OUTFMT=pct -NORM=ext -HEAPSIZE=500 -MINLEN=0
-NCPU=6 -ICPU=3 -NO_MMAP -LARGQUERY -NEG_SCORES=0 -WAIT -DSHLOCK=100
-LONGLOG -DEV_TIMEOUT=120 -WARN_TIMEOUT=10 -THREADS=1 -XGAPOP=10 -XGAPEXT=0.5
-FGAPOP=6 -FGAPEXT=7 -YGAPOP=10 -YGAPEXT=0.5 -DELOP=6 -DELEXT=7

Database : Published Applications NA:
1: /cgn2_6/ptodata/1/pubpna/US07_PUBCOMB.seq:*
2: /cgn2_6/ptodata/1/pubpna/PCT_NEW_PUB.seq:*
3: /cgn2_6/ptodata/1/pubpna/US06_NEW_PUB.seq:*
4: /cgn2_6/ptodata/1/pubpna/US07_NEW_PUB.seq:*
5: /cgn2_6/ptodata/1/pubpna/US06_PUBCOMB.seq:*
6: /cgn2_6/ptodata/1/pubpna/PCTUS_PUBCOMB.seq:*
7: /cgn2_6/ptodata/1/pubpna/US08_NEW_PUB.seq:*
8: /cgn2_6/ptodata/1/pubpna/US08_PUBCOMB.seq:*
9: /cgn2_6/ptodata/1/pubpna/US09_PUBCOMB.seq:*
10: /cgn2_6/ptodata/1/pubpna/US09B_PUBCOMB.seq:*
11: /cgn2_6/ptodata/1/pubpna/US09C_PUBCOMB.seq:*
12: /cgn2_6/ptodata/1/pubpna/US09C_PUBCOMB.seq:*
13: /cgn2_6/ptodata/1/pubpna/US09_NEW_PUB.seq:*
14: /cgn2_6/ptodata/1/pubpna/US10_PUBCOMB.seq:*
15: /cgn2_6/ptodata/1/pubpna/US10B_PUBCOMB.seq:*
16: /cgn2_6/ptodata/1/pubpna/US10C_PUBCOMB.seq:*
17: /cgn2_6/ptodata/1/pubpna/US10D_PUBCOMB.seq:*
18: /cgn2_6/ptodata/1/pubpna/US10E_PUBCOMB.seq:*
19: /cgn2_6/ptodata/1/pubpna/US10F_PUBCOMB.seq:*
20: /cgn2_6/ptodata/1/pubpna/US10G_PUBCOMB.seq:*
21: /cgn2_6/ptodata/1/pubpna/US10H_PUBCOMB.seq:*
22: /cgn2_6/ptodata/1/pubpna/US10I_PUBCOMB.seq:*
23: /cgn2_6/ptodata/1/pubpna/US10J_NEW_PUB.seq:*
24: /cgn2_6/ptodata/1/pubpna/US10K_NEW_PUB.seq:*
25: /cgn2_6/ptodata/1/pubpna/US11_PUBCOMB.seq:*
26: /cgn2_6/ptodata/1/pubpna/US11_NEW_PUB.seq:*
27: /cgn2_6/ptodata/1/pubpna/US60_NEW_PUB.seq:*
28: /cgn2_6/ptodata/1/pubpna/US60_PUBCOMB.seq:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
C 1	1380	100.0	11204	22 US-10-893-671-30	Sequence 30, Appl
C 2	937	67.9	640681	9 US-09-790-988-1	Sequence 1, Appl
C 3	911.5	66.1	908766	24 US-10-795-159-685	Sequence 665, App
C 4	910.5	66.0	807	24 US-10-958-216-120	Sequence 120, App
C 5	910.5	66.0	1830121	18 US-10-329-670-1	Sequence 1, Appl
C 6	910.5	66.0	1830121	21 US-10-158-863-1	Sequence 1, Appl
C 7	910.5	66.0	1830121	24 US-10-981-687-1	Sequence 1, Appl
C 8	909.5	65.9	786	24 US-10-958-216-58	Sequence 58, Appl
C 9	909.5	65.9	786	24 US-10-958-216-60	Sequence 60, Appl
C 10	904.5	65.5	807	24 US-10-958-216-122	Sequence 122, App
C 11	852	61.7	2731748	20 US-10-297-465A-1	Sequence 1, Appl
C 12	799.5	57.9	96109	19 US-10-672-787-35	Sequence 35, Appl
C 13	758.5	55.0	92934	24 US-10-915-740A-21	Sequence 21, Appl
C 14	758.5	55.0	2242716	24 US-10-915-740A-1068	Sequence 1068, App
C 15	619	44.9	855	16 US-10-156-761-5908	Sequence 5908, App
C 16	619	44.9	9025608	16 US-10-156-761-1	Sequence 1, Appl
C 17	617.5	44.7	1735	21 US-10-425-115-11629	Sequence 11629, App
C 18	614	44.5	2671	18 US-10-299-867-1	Sequence 1, Appl
C 19	614	44.5	2671	21 US-10-723-860-1102	Sequence 1102, App
C 20	614	44.5	2984	18 US-10-399-645-28	Sequence 28, Appl
C 21	597.5	43.3	3309400	9 US-09-738-626-1	Sequence 1, Appl
C 22	595.5	43.2	789	9 US-09-738-626-2198	Sequence 2198, App
C 23	595	43.1	1125	26 US-11-097-143-31928	Sequence 31928, A
C 24	594	43.0	1197	9 US-09-938-842A-2427	Sequence 2427, App
C 25	594	43.0	1197	11 US-09-938-842A-2427	Sequence 2427, App
C 26	590	42.8	747	9 US-09-974-300-1195	Sequence 1195, App
C 27	590	42.8	1747	24 US-10-510-812-33	Sequence 33, Appl
C 28	587	42.5	1165	19 US-10-424-599-104571	Sequence 104571, App
C 29	574.5	41.6	1165	17 US-11-032-588-6697	Sequence 6697, App
C 30	571.5	41.4	2287	26 US-11-097-143-31924	Sequence 31924, A
C 31	571.5	41.4	3262	26 US-11-097-143-31927	Sequence 31927, A
C 32	565.5	41.0	1360	21 US-10-425-115-452	Sequence 452, App
C 33	562.5	40.8	1295	19 US-10-425-115-2639	Sequence 2639, A
C 34	557.5	40.4	1306	20 US-10-437-963-48139	Sequence 48139, A
C 35	552.5	40.0	3088	21 US-10-723-860-5641	Sequence 5641, App
C 36	550.5	39.9	1534	19 US-10-424-599-30704	Sequence 30704, A
C 37	547.5	39.7	1889	21 US-10-425-115-168772	Sequence 168772, A
C 38	547.5	39.7	1489	20 US-10-437-963-68096	Sequence 68096, A
C 39	539	39.1	1230025	18 US-10-289-762-1	Sequence 1, Appl
C 40	531.5	38.5	1525	19 US-10-424-599-101159	Sequence 101159, App
C 41	519	37.6	762	24 US-10-958-216-102	Sequence 102, App
C 42	519	37.6	1856	9 US-09-070-927A-494	Sequence 494, App
C 43	518.5	37.6	943	26 US-11-097-143-10796	Sequence 10796, A
C 44	518.5	37.6	1734	21 US-10-425-115-114723	Sequence 114723, A
C 45	516	37.4	807	24 US-10-501-282-3477	Sequence 3477, App

ALIGNMENTS

RESULT 1
US-10-893-671-30/c
; Sequence 30, Application US/10893671
; Publication No. US20050064527A1
; GENERAL INFORMATION:
; APPLICANT: Levy, Stuart, et. al.
; TITLE OF INVENTION: NMR COMPOSITIONS AND THEIR METHODS OF USE
; FILE REFERENCE: PKZ-043
; CURRENT APPLICATION NUMBER: US/10/893,671
; PRIOR FILING DATE: 2004-07-15
; PRIOR APPLICATION NUMBER: US/09/801,563
; PRIOR FILING DATE: 2001-03-08
; PRIOR APPLICATION NUMBER: 60/188,362
; PRIOR FILING DATE: 2000-03-10

OM protein - nucleic search, using frame_plus_p2n model

Run on: November 11, 2005, 18:19:03 ; Search time 145 Seconds

(without alignments)
2979.152 Million cell updates/sec

Title: US-10-813-549-1
Perfect score: 1380
Sequence: 1 MA5IKTPEDERKRVAGRL.....CEITTKRDTTPAISHDE 264

Scoring table:
BIOSUM62
Xgapop 10.0 , Xgapext 0.5
Ygapop 10.0 , Ygapext 0.5
Fgapop 6.0 , Fgapext 7.0
Delop 6.0 , Delext 7.0

Searched: 1202784 seqs, 818138359 residues

Total number of hits satisfying chosen parameters: 2405568

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Command line parameters:
-MODEL=frame+ p2n.model -DEV=x1h
-O=/cg2_1/USPTO.spool/US10813549/runat_03112005_075936.13189/app.query.fasta_1.455
-DB=Issued Patents NA -OPMT=fastcap -SUFFIX=rni -MINMATCH=0.1 -LOOFC=0
-LOOPEXT=0 -UNITS=bits -START=1 -END=1 -MATRIX=bloesum2 -TRANS=human40.cdi
-LIST=45 -DOCLIGN=200 -THR.SCORB=pct -THR.MAX=100 -THR.MIN=0 -ALIGN=20
-MODE=LOCAL -OUTFMT=pct -NOM=ext -HEAPSIZE=500 -MINLEN=0 -MAXLEN=2000000000
-USER=US10813549.@CG2_1.1_69@runat_03112005_075936.13189 -NCPU=6 -ICPU=3
-NOM WMAP -LARGEQUERY -NEG SCORES=0 -WAIT -DSPLOCK=100 -LONGLOG
-DEV TIMEOUT=120 -MARN TIMEOUT=30 -THREDS=1 -XGAPOP=10 -XGAPEXT=0.5 -FGAPOP=6
-FGAPEXT=7 -YGAPOP=10 -YGAPEXT=0.5 -DELOP=6 -DELEXT=7

Database:

Issued Patents NA:
1: /cg2_6/ptodata/1/ina/5A.COMB.seq:*
2: /cg2_6/ptodata/1/ina/5B.COMB.seq:*
3: /cg2_6/ptodata/1/ina/6A.COMB.seq:*
4: /cg2_6/ptodata/1/ina/6B.COMB.seq:*
5: /cg2_6/ptodata/1/ina/PTUS.COMB.seq:*
6: /cg2_6/ptodata/1/ina/backfile1.seq:*

Pred. No. is the number of results predicted by the chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	1380	96.4	846	4	US-09-489-039A-5218 Sequence 5218, Ap
2	1086	78.7	807	4	US-09-543-681A-2424 Sequence 2424, Ap
3	937	67.9	640681	4	US-09-790-988-1 Sequence 1, Appli
4	910.5	66.0	1830121	4	US-09-557-884-1 Sequence 1, Appli
5	910.5	65.9	858	4	US-09-643-990A-1 Sequence 1, Appli
6	909.5	65.9	963	4	US-09-252-991A-4171 Sequence 4171, Ap
7	909.5	65.9	963	4	US-09-252-991A-4435 Sequence 4435, Ap
8	909.5	65.9	1176	4	US-09-252-991A-4314 Sequence 4314, Ap
9	824.5	57.9	861	4	US-09-328-352-308 Sequence 308, Ap
10	799.5	57.9	807	4	US-09-540-236-657 Sequence 657, Ap
11	799.5	57.9	96109	4	US-09-596-002-35 Sequence 35, Appli
12	798	57.8	795	4	US-09-328-352-3450 Sequence 3450, Ap

13	739	53.6	912	4	US-09-252-991A-14700 Sequence 14700, A
14	739	53.6	1125	4	US-09-252-991A-14568 Sequence 14568, A
15	739	53.6	1248	4	US-09-252-991A-15057 Sequence 15057, A
16	701	50.8	798	4	US-09-543-681A-3675 Sequence 3675, Ap
17	682	49.4	2706	3	US-09-066-046-23 Sequence 23, Appli
18	617	44.7	852	4	US-09-902-540-4170 Sequence 4170, Ap
19	617	44.7	18686	4	US-09-902-540-1206 Sequence 1206, Ap
20	617	44.7	4403765	3	US-09-103-840A-2 Sequence 2, Appli
21	617	44.7	4411529	3	US-09-103-840A-1 Sequence 1, Appli
22	614	44.5	2671	4	US-09-523-263B-1 Sequence 1, Appli
23	597.5	43.3	996	4	US-09-602-777A-35 Sequence 35, Appli
24	575	41.7	1239	4	US-09-270-767-10002 Sequence 10002, A
25	552.5	40.0	783	4	US-09-902-540-5059 Sequence 5059, Ap
26	552.5	40.0	30135	4	US-09-902-540-1249 Sequence 1249, Ap
27	539	39.1	123025	4	US-09-198-452A-1 Sequence 1, Appli
28	539	39.1	1230230	4	US-09-438-185A-1 Sequence 1, Appli
29	489.5	35.5	1529	4	US-09-523-263B-7 Sequence 7, Appli
30	489.5	35.5	1798	3	US-09-797-906-1 Sequence 1, Appli
31	489.5	35.5	3064	4	US-09-620-312D-378 Sequence 378, App
32	489.5	35.5	3114	4	US-09-523-263B-5 Sequence 5, Appli
33	473	34.3	618	4	US-09-489-039A-2229 Sequence 2229, Ap
34	450.5	32.6	1039	3	US-08-975-762-16 Sequence 36, Appli
35	450.5	32.6	1039	3	US-08-821-324-36 Sequence 36, Appli
36	450.5	32.6	1039	3	US-09-295-028-36 Sequence 36, Appli
37	450.5	32.6	1039	3	US-09-106-582-36 Sequence 36, Appli
38	450.5	32.6	1039	4	US-09-159-469-36 Sequence 36, Appli
39	450.5	32.6	1039	4	US-09-693-542-36 Sequence 36, Appli
40	450.5	32.6	3073	3	US-08-975-762-41 Sequence 41, Appli
41	450.5	32.6	3073	3	US-09-295-028-41 Sequence 41, Appli
42	450.5	32.6	3073	3	US-09-106-582-41 Sequence 41, Appli
43	450.5	32.6	3073	4	US-09-159-469-41 Sequence 41, Appli
44	450.5	32.6	3073	4	US-09-693-542-41 Sequence 41, Appli
45	446.5	32.4	756	4	US-09-710-279-1895 Sequence 1895, Ap

ALIGNMENTS

RESULT 1
US-09-489-039A-5218
Sequence 5218, Application US/09489039A
Patent No. 6610836
GENERAL INFORMATION:
APPLICANT: Gary Breton et. al
TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO KLEBSIELLA
FILE REFERENCE: PNEUMONIAE FOR DIAGNOSTICS AND THERAPEUTICS
CURRENT APPLICATION NUMBER: 2709.2004001
CURRENT FILING DATE: 2000-01-27
PRIOR APPLICATION NUMBER: US/09/489,039A
PRIOR FILING DATE: 1999-01-29
NUMBER OF SEQ ID NOS: 14342
SEQ ID NO 5218
LENGTH: 846
TYPE: DNA
ORGANISM: Klebsiella pneumoniae
US-09-489-039A-5218

Alignment Scores:

Pred. No.: 2.02e-174
Score: 1330.00
Percent Similarity: 97.73%
Best Local Similarity: 96.21%
Query Match: 96.38%
DB: 4
Length: 846
Matches: 254
Conservative: 4
Mismatches: 6
Indels: 0
Gaps: 0

US-10-813-549-1 (1-264) x US-09-489-039A-5218 (1-846)
Qy 1 MetAlaIleSerIleThrProGluAaPIIleGluIleMetArgValaIaGIArgLeu 20
Db 52 ATGGCATCTCTATTAGACATCTGAAACATCGAAAAATGCGCTTGGCCGCGCTG 111
Qy 21 AAlaAGIValleuGIuMetIleGIuProIyValIleProGIyValSerThryGIu 40

OM protein - nucleic search, using frame_plus_p2n model

Run on: November 11, 2005, 14:27:17 ; Search time 406 Seconds

(without alignments)
3849.290 Million cell updates/sec

Title: US-10-813-549-1

Sequence: 1 MAISIKTPEDIEKRVAGRL.....CEILTLRKDDTTPALISHDE 264

Scoring table:

BLOSUM62
Xgapop 10.0 , Xgapext 0.5
Ygapop 10.0 , Ygapext 0.5
Fgapop 6.0 , Fgapext 7.0
Delop 6.0 , Delext 7.0

Searched: 4390206 seqs, 2959870667 residues

Total number of hits satisfying chosen parameters: 8780412

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Command line parameters:

-MODE=frame+ p2n.model -DEV=x1h
-O=/cgn2_1/USPTO_SPOOL/US10813549/runat_03112005_075935_1156/app_query.fasta.1.455
-DB=N_Geneseq_16Dec04 -OPMT=faesap -SUFFIX=ring -MINMATCH=0.1 -LOOFCU=0
-LOOPEXT=0 -UNITS=bits -START=1 -END=1 -MATRIX=blousum62 -TRANS=human40.cdi
-LIST=45 -DOCALLIGN=200 -THR_SCORE=PCT -THR_MAX=100 -THR_MIN=0 -ALIGN=20
-MODE=LOCAL -OUTFMT=PCT -NORM=ext -HEAPSIZE=500 -MINLEN=0 -MAXLEN=2000000000
-USER=US10813549_@CGN 1 1 470 @runat_03112005_075935_1156 -NCPU=6 -ICPU=3
-NO_MMAP -LARGEQUERY -NEG_SCORES=0 -WAIT -DSPBLOCK=100 -LONGLOG
-DEV TIMEOUT=120 -MAIN TIMEOUT=30 -THREADS=1 -XGAPOP=10 -XGAPEXT=0.5 -FGAPOP=6
-FGAPEXT=7 -YGAPOP=10 -YGAPEXT=0.5 -DELOP=6 -DELEXT=7

Database:

N_Geneseq_16Dec04:*
1: geneseqn1980s:*
2: geneseqn1990s:*
3: geneseqn2000s:*
4: geneseqn2001as:*
5: geneseqn2001bs:*
6: geneseqn2002as:*
7: geneseqn2002bs:*
8: geneseqn2003as:*
9: geneseqn2003bs:*
10: geneseqn2003cs:*
11: geneseqn2003ds:*
12: geneseqn2004as:*
13: geneseqn2004bs:*

Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	1380	100.0	1197	1	AAAN70151
2	1380	100.0	11204	4	AAAS46245
3	1330	96.4	846	11	ACH99423
4	1137.5	82.4	798	10	ACF69733
5	1137.5	82.4	110000	10	ACF67367_27

C	6	1137.5	82.4	110000	10	ACF65386_1	Continuation (2 of
C	7	1086	78.7	807	10	ADF02139	Adf02139 Bacterial
C	8	937	67.9	110000	6	ABA92787_2	Continuation (3 of
C	9	911.5	66.1	308766	13	ADT05738	Adt05738 Haemophil
C	10	910.5	66.0	807	10	ADG73412	Adg73412 Haemophil
C	11	910.5	66.0	110000	2	AA742063_17	Continuation (18 o
C	12	909.5	65.9	786	10	ADG73350	Adg73350 Pseudomon
C	13	909.5	65.9	786	10	ADG73352	Adg73352 Pseudomon
C	14	909.5	65.9	858	11	ABD05567	Abd05567 Pseudomon
C	15	909.5	65.9	963	11	ABD05831	Abd05831 Pseudomon
C	16	909.5	65.9	1176	11	ABD05710	Abd05710 Pseudomon
C	17	904.5	65.5	807	10	ADG73414	Adg73414 Haemophil
C	18	824.5	59.7	807	10	ADA29021	Ada29021 DNA encod
C	19	799.5	57.9	807	12	ADL02971	Adl02971 DNA encod
C	20	799.5	57.9	96109	4	AAF28548	AAF28548 Genomic f
C	21	798	57.8	795	9	ADA32163	Ada32163 DNA encod
C	22	758.5	55.0	92934	3	AAA81473	Continuation (8 of
C	23	758.5	55.0	110000	3	AAA81489_7	Continuation (8 of
C	24	758.5	55.0	172325	3	AAF21613	AAF21613 Neisseria
C	25	739	53.6	912	11	ABD16096	Abd16096 Pseudomon
C	26	739	53.6	1125	11	ABD15964	Abd15964 Pseudomon
C	27	739	53.6	1248	11	ABD16453	Abd16453 Pseudomon
C	28	701	50.8	798	10	ADF03390	Adf03390 Bacterial
C	29	682	49.4	2706	2	AAV81790	AAV81790 Granulocy
C	30	618.5	44.8	645	10	AB237943	AB237943 N. gonorr
C	31	617	44.7	110000	4	AAI99682_31	Continuation (32 o
C	32	617	44.7	110000	4	AAI99682_31	Continuation (32 o
C	33	616.5	44.7	1625	3	AA644483	AA644483 Zea mays
C	34	614.5	44.5	1578	3	AA643773	AA643773 Zea mays
C	35	614	44.5	2671	10	ADG44828	Adg44828 Human CDN
C	36	614	44.5	2671	10	ADG42842	Adg42842 Human met
C	37	614	44.5	2671	12	AD018284	Adg18284 Human sof
C	38	614	44.5	2984	6	ABK86146	ABK86146 CDNA enco
C	39	597.5	43.3	996	4	AAH71155	AAH71155 Corynebact
C	40	597.5	43.3	349980	5	AAH68531	AAH68531 C glutami
C	41	597.5	43.3	349980	5	AAH68530	AAH68530 C glutami
C	42	595.5	43.2	789	5	AAH67163	AAH67163 C glutami
C	43	595	43.1	1125	4	ABL23125	ABL23125 Drosophil
C	44	594	43.0	1197	6	ABZ16622	ABZ1622 Arabidops
C	45	594	43.0	1419	13	ADR42904	ADR42904 Arabidops

ALIGNMENTS

RESULT 1	
AAAN70151	
ID	AAAN70151 standard; DNA; 1197 BP.
XX	
XX	AAAN70151;
XX	
DT	09-APR-1991 (first entry)
XX	
DE	Insert of psyc1174 encoding Met-aminopeptidase.
XX	
XX	Met-aminopeptidase; antibody.
KM	
XX	
OS	Escherichia coli.
XX	
FH	
FT	Key
FT	CDS
XX	Location/Qualifiers
XX	219..1013
XX	/*tag= a
PN	EP219237-A.
XX	
PD	22-APR-1987.
XX	
PF	19-SEP-1986; 86EP-00307242.
XX	
PR	20-SEP-1985; 85US-00778414.
XX	
XX	06-MAY-1986; 86US-00860330.
XX	
PA	(CETU) CETUS CORP.
XX	